Shawn Shaw #65939-050

FCI Elkton

P.O. Box 10

Lisbon, Ohio 44430

12/12/2020

RE: United States v. Shawn Shaw, case no. 2:19-cv-16702

Dear Clerk of the Court,

Enclosed is a Declaration and Affidavit to be filed in the above case as "Petitioner's Exhibit C: Declaration of Arthur Young and exhibit D: Affidavit of Arthur Young." Thank you for your time.

Respectfully,

Shawn Shaw #65939-050

FCI Elkton

P.O. Box 10

Lisbon, Ohio 44430

UNITED STATES DISTRICT COURT
DISTRICT OF NEW JERSEY

SHAWN D. SHAW	:	HON. ESTHER SALAS Civ. No. 19-16702
v.	:	AFFIDAVIT
UNITED STATES OF AMERICA	:	

AFFIDAVIT IN SUPPORT OF SHAWN SHAW'S MOTION TO VACATE, SET ASIDE, OR CORRECT HIS SENTENCE UNDER 28 U.S.C. § 2255

I, Arthur Young, of full age, being duly sworn upon my oath, certify as to the following:

1. I have been retained to review discovery and information and render an opinion with respect to forensic evidence sought to be used at the trial of the above Defendant, Shawn Shaw.
2. I am a Forensic Biologist Specialist and Managing Partner of Guardian Forensic Sciences.
3. Guardian Forensic Sciences is a privately-held forensic laboratory, and is accredited by the ANAB (ANSI (American National Standards Institute) National Accreditation Board).
4. Prior to Guardian Forensic Sciences, I held positions at two other laboratories: I was a forensic biologist at NMS Labs in Willow Grove, Pennsylvania, from 2002-2010, and a forensic chemist at Acadiana Criminalistics Laboratory in New Iberia, Louisiana, from 1991-2001. In addition, I was an adjunct instructor in Forensic Biology at Arcadia University in Glenside, Pennsylvania from 2004-2008.

5. I earned my Bachelor of Science in 1991 from the University of Southwestern Louisiana in Lafayette, Louisiana (renamed to the University of Louisiana at Lafayette), having majored in Pre-Medical Sciences.
6. I have attended training at the Federal Bureau of Investigation, the Serological Research Institute, and the McCrone Research Institute, as well as maintain continuing education and training via workshops and conferences, as well as reading peer-reviewed scientific journals.
7. I continue to maintain my skills through independent proficiency testing in forensic serology, forensic DNA analysis, and blood stain pattern interpretation.
8. I am a Fellow with, and certified by, the American Board of Criminalistics, including a technical specialty in Molecular Biology.
9. I am a member of the American Academy of Forensic Sciences, the Mid-Atlantic Association of Forensic Scientists, the Southern Association of Forensic Scientists, the Association of Forensic DNA Analysts and Administrators, and the International Association of Bloodstain Pattern Analysts.
10. I have been qualified as an expert in the following practice areas: Forensic serology, forensic DNA analysis, forensic biology, and blood stain pattern interpretation in both state and federal courts. Prior to the utilization of forensic DNA analysis, I was trained and proficient in the forensic serologic methods of the era, which include the forensic identification of bodily fluids, ABO typing of liquid blood, of blood stains, and of non-blood stains such as semen and saliva stains.
11. I regularly lecture at professional conferences and meetings throughout the United States and abroad, and for law enforcement and legal organizations, as well as civic groups.
12. Based on my background and experience, I have been permitted to render opinions as a forensic expert in Arkansas, California, Delaware, Florida, Georgia, Louisiana, Maryland, Massachusetts, New Jersey, New York, Pennsylvania, Texas, Virginia, West Virginia, Wisconsin, and the District of Columbia.
13. My current *curriculum vitae* (CV), which fairly represents my education, experience, and training, is attached and incorporated to this affidavit (see Exhibit A).
14. Advice to counsel – In my original conversations with Mr. Anthony Mack, he had expressed that he wanted a brief letter that outlined the issues that I would discuss (see Exhibit B); it was not necessary to go into great detail, as many issues could be asked on direct examination of the State's expert and did not require my opinion.
15. I never made any statement to either Mr. Mack or Mr. Fury that I should or should not testify. That is a decision for the attorney to make, not the expert. In either case, my role is to assist the attorney

with trial preparation, in whatever manner he or she decides. This is a basic part of an attorney's trial strategy, and I do not presume any role outside of my own.

16. State's Brief – In addition to the files that I originally received, I have read the document, "Brief of the United States in Opposition to Shawn Shaw's Motion to Vacate, Set Aside, or Correct His Sentence Under 28 U.S.C. § 2255." In several points throughout the Brief, the State attempts to mischaracterize what my testimony would have been. I seek to rectify those issues in this affidavit.

17. One of the most egregious mischaracterizations is on page 22, where it states, *"Young concedes in his report that Nezezon's decision to include of D13S17 [sic] had support in the forensic community, though he would have used more conditional language in stating the likelihood ratio. Id. Thus, even if Young had testified, he would have likely conceded that Nezezon's methodologies, though perhaps not what he would have used, had support in the scientific community."* I made no such statement in my single-paged letter, dated 05/07/14 (see Exhibit B). The statement was made, however, in an email to Mr. Mack, dated 05/02/14 (see Exhibit C), where I wrote, *"The problem is that, in this case, the DNA data isn't complete. Foreign DNA was detected at only five of the sixteen genetic markers that were analyzed (D8S1179, D3S1358, TH01, vWA, and D5S818). However, at a sixth genetic marker (D13S317), Strife has alleles 9 and 12 while Shaw has a 12. At this marker, a 9 and a 12 were detected; Shaw's 12 might be here, but it also may not - we call this situation "masking", where one person's alleles are hidden by the other person. The question that I had was, "Was this genetic marker used in the calculation?" This is very important because the lab would have been using that portion of the evidentiary data against Mr. Shaw, even though there was no proof of him being present (see "SHAW 000179", which is the electropheragrammic data for this sample). Basically, you could only arrive at their conclusion if you assumed that Mr. Shaw's DNA is present, whereby, you would also have to assume that he's guilty. That is not a practice that the lab should be engaging in. However, I do understand it and there are some forensic scientists who advocate the practice. If the NJSP lab wants to use this method, they have some support in this field. What they DON'T have is the conditional language that is supposed to surround the likelihood ratio figures, and that changes the rules of the game."* It is not clear to me how the State came to be in possession of this email, or why it was falsely attributed to my "report." As a single email, however, it was not meant to be all-inclusive or for anyone else's attention, nor does it represent the full context of our conversations up to that point in time. The merits of these statements are discussed in Paragraphs 20 through 30, and 35.

18. The State acknowledges that it is in possession of said email on page 17 when it writes, *"Young summarized his opinion in an email to Attorney Mack dated May 2, 2014 and in a letter dated May 7, 2014. See id."*

19. The same mischaracterization continues, on pages 22-23, where it states, *"As to the likelihood ratio, Young noted that he was unable to "backcalculate and remove [the D13S17 [sic] locus], as [he] [didn't] have the exact numbers" that Nezezon used. Id. Accordingly, he broadly concluded, "you can expect to have gone down by a factor of ten." Id. This speculation is incorrect. As Nezezon set forth in her declaration, when the D13S17 [sic] locus is removed from the calculation, the likelihood ratio for the autosomal analysis is approximately 1,860, which is still above the 1,000 threshold for very strong support, per the seminal DNA textbook. Nezezon Decl., attached hereto as Ex. 2, ¶ 5."* Again, I made no such statement in my letter, dated 05/07/14 (see Exhibit B), but rather, in the same email to Mr. Mack, dated 05/02/14 (see Exhibit C), where I wrote, *"The statistical calculations (see "SHAW 000195") show that D13S317 was used in the calculation. I cannot backcalculate and remove that marker, as I don't have the exact numbers that they plugged in. However, you can expect to have gone down by a factor of ten ("900 times more likely", versus "9,000 times more likely"). By doing so, there is a bias present that was used to inflate the numbers against the defendant."* My statement was meant solely for the purposes of the email, in order to convey to Mr. Mack the mathematical effect of including or excluding a locus would have had, and was not meant to be an authoritative statement on the matter, as I did not have the NJSP's citation in front of me at the time that the email was composed. The merits of these statements are discussed in Paragraph 26. Furthermore, if the revised frequency went from 9,090 to 1,860 (I have not seen Ms. Nezezon's declaration, nor does the State's Brief specify which race the 1,860 value applies to), then that's a 4.89-fold difference, which is not that far off from my ten-fold rule-of-thumb.

20. Forensic DNA STR Analysis – In summary, while it was not possible to exclude Mr. Shaw as the source of the six foreign alleles that were detected (D8S1179:14; D3S1358:16; TH01:8; vWA:17; D5S818:11; and FGA:22), six alleles do not constitute a DNA match. In addition, these six foreign alleles were detected at a distinct but minute level. This is relevant for numerous reasons.

21. Many DNA mixtures can be deconvoluted, meaning that the constituent DNA profiles that contributed to the mixture can be determined with fair accuracy. Ideally, the mixture should be a ratio of 1:2, down to about 1:8. Beyond that, there can be risks of allelic drop-out, but also misidentification of an amplification artifact known as "stutter." Stutter is always one repeat unit less than, and a certain percentage of, the parent peak that created it, like a shadow; when the foreign alleles are small and in stutter positions, extreme caution should be applied. Of the six foreign

alleles indicated above, five of them are in stutter positions. The following is an excerpt from page 3 of the report dated 11/01/11, which shows, for both Specimen #1-1 (SCF) and #1-2 (SCF):

- the five alleles that are in stutter position (boxed),
- the one that is not in stutter position (circled), and
- the asterisks, indicating *"[a]dditional allele(s) were obtained at this locus which were below the reporting threshold of this laboratory."* (arrows).

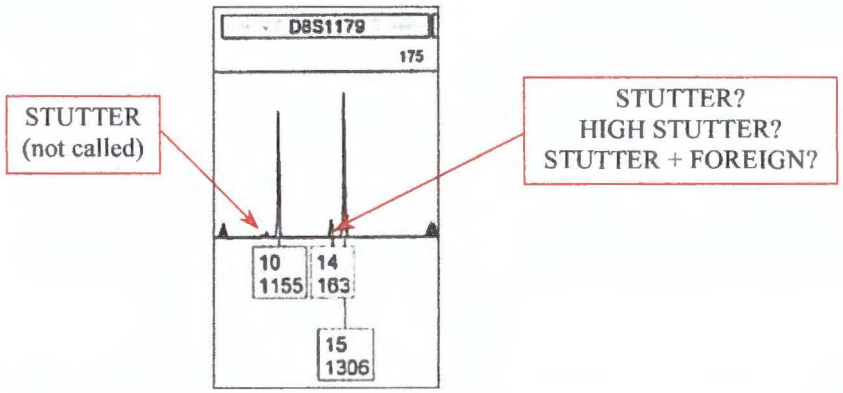
Specimen No.	Specimen Description	Human DNA Probe	D8S1179	D21S11	D7S820	CSF1PO	D3S1358	TH01	D13S317	D16S539	D2S1338	D19S433	VWA	TPOX	D18S51	Amelogenin	D5S818	FGA
2	Buccal Swab Reference (S)	+	14,15	30,32	10,11	10,13	16,17	8,8	12,12	11,12	21,24	12,14	17,18	7,8	15,19	X,Y	11,12	22,24
1-5	Buccal Swab Reference (V) (Previously reported 5/2/11)		10,15	28,33.2	9,9	12,12	15,17	6,6	9,12	9,11	18,20	14,14	16,18	8,11	15,17	X,X	10,12	19,23
1-1 (SCF)	Vaginal Swabs (V) (Previously reported 5/2/11)		10,15 (14)	28,33.2*	9,9	12,12	15,17 (16)	6,6 (8)	9,12	9,11	18,20	14,14*	16,18 (17)	8,11	15,17	X,X*	10,12 (11)	19,23 (22)
1-1 (NSCF)	Vaginal Swabs (V) (Previously reported 5/2/11)		10,15	28,33.2	9,9	12,12	15,17	6,6	9,12	9,11	18,20	14,14	16,18	8,11	15,17	X,X	10,12	19,23
1-2 (SCF)	Cervical Swabs (V) (Previously reported 5/2/11)		10,15 (14)	28,33.2	9,9	12,12	15,17 (16)	6,6 (8)	9,12	9,11	18,20	14,14*	16,18 (17)	8,11	15,17	X,X	10,12 (11)	19,23
1-2	Cervical Swabs (V) (Previously																	

Each of these issues will be discussed in the following paragraphs.

22. The following is an excerpt from page 3 of the report dated 11/01/11, which shows that Specimen #1-1 (SCF) and #1-2 (SCF) were conflated into a single conclusion, as if their results were identical:

> **CONCLUSIONS & INTERPRETATIONS**
>
> A mixture of DNA profiles was identified in Specimens No. 1-1 (SCF) and 1-2 (SCF). Emily Strife and Shawn D. Shaw cannot be excluded as partial contributors to the mixed DNA profile obtained. Assuming two contributors, one of whom is Emily Strife, it is approximately:
>
> 9.09 thousand times more likely in the African-American population
> 19.0 thousand times more likely in the Caucasian population
> 14.1 thousand times more likely in the Hispanic population
>
> that the source of the mixed DNA profile is Emily Strife and Shawn D. Shaw rather than Emily Strife and a randomly selected individual.

23. Although the five alleles in stutter positions are greater than the prescribed limit for observed stutter with the Identifiler DNA amplification kit, the heights of the peaks are not all to be attributed to a foreign contributor, either; some portion of the peak's height is still due to stutter – what remains may be attributed to a foreign contributor. The first locus, D8S1179, will be considered, where the "10" allele shows a tiny peak to the left (which was not called), as well as the "(14)" allele, which is in stutter position to the parent 15 peak:



The following is an excerpt from page 7-18 of Version 2010 of the DNA STR Protocol Manual of the New Jersey State Police's Office of Forensic Sciences (see Exhibit D), which prescribes both the average percent stutter for each locus for the Identifiler DNA Amplification Kit, as well as the maximum percent stutter (determined by average ± three standard deviations):

% (n-4) Stutter for Identifiler Loci

Locus	D8S1179	D21S11	D7S820	CSF1PO	D3S1358	TH01	D13S317	D16S539
Max % Stutter	7.13	8.03	7.73	7.16	9.4	5.42	7.29	8.92
Avg. % Stutter	4.84	5.25	3.92	4.14	5.61	2.44	4.04	4.77
Locus	D2S1338	D19S433	vWA	TPOX	D18S51	D5S818	FGA	
Max % Stutter	11.67	10.03	10.44	5.0	13.21	7.57	11.2	
Avg. % Stutter	6.71	6.77	5.58	2.48	7.81	4.29	6.37	

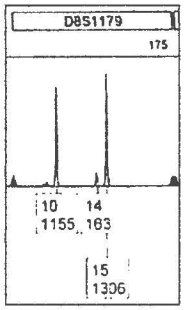
Peaks in the stutter position that exceed the maximum percent stutter at a particular locus may be designated as a true allele. Peaks that exceed the maximum percent stutter at a particular locus but that may be attributable to stutter should be enclosed in { }.

The chart prescribes that the average stutter percentage for locus D8S1179 is 4.84%, with a maximum percentage of 7.13%. Therefore, the expected stutter peak is expected to be 63 RFUs (relative fluorescent units)(1,306 RFUs x 4.84%), and no more than 93 RFUs (1,306 RFUs x 7.13%). The 14 allele has a peak height of 163 RFUs, which means that approximately 100 RFUs (163 RFUs – 63 RFUs) cannot be explained as being from stutter, but that difference may be as little as 70 RFUs (163 RFUs – 93 RFUs). However, just because a peak is above the average stutter percentage doesn't mean that the peak is, at least in part, stutter; stutter always happens.

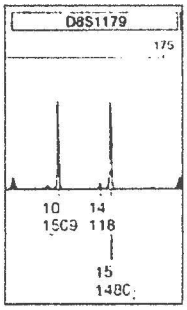
Page 7-7 of Version 2010 of the DNA STR Protocol Manual of the New Jersey State Police's Office of Forensic Sciences (see Exhibit E) states, *"Peaks must be 100 RFU (reporting threshold) or greater to be considered conclusive for match purposes."* Stated another way, stutter artificially elevated alleles into a callable range, although no apparent consideration appears to have been taken to account for it. Additionally, the DNA STR Protocol Manual indirectly acknowledges that stutter can still exceed the maximum observed percentage: *"Peaks that exceed the maximum percent stutter at a particular locus but that may be attributable to stutter should be enclosed in { }."* Having explained this process, this locus, as well as the remaining four loci, are easier to see in a tabular format:

D8S1179

#1-1 (SCF)	IF STUTTER IS AT AVERAGE PERCENTAGE	IF STUTTER IS AT MAXIMUM OBSERVED PERCENTAGE
PARENT PEAK HEIGHT (CALL)	1,306 RFUs (15)	1,306 RFUs (15)
QUESTIONED PEAK HEIGHT (CALL)	163 RFUs (14)	163 RFUs (14)
STUTTER PEAK HEIGHT PERCENTAGE	4.84%	7.13%
CALCULATED STUTTER PEAK HEIGHT	63 RFUs	93 RFUs
REMAINDER ATTRIBUTABLE TO FOREIGN SOURCE	100 RFUs	70 RFUs
DEEMED ACCEPTABLE? (*i.e.*, ≥100 RFUs)	Yes	No



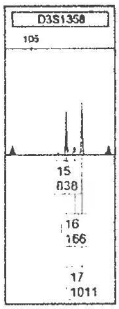
#1-2 (SCF)	IF STUTTER IS AT AVERAGE PERCENTAGE	IF STUTTER IS AT MAXIMUM OBSERVED PERCENTAGE
PARENT PEAK HEIGHT (CALL)	1,480 RFUs (15)	1,480 RFUs (15)
QUESTIONED PEAK HEIGHT (CALL)	118 RFUs (14)	118 RFUs (14)
STUTTER PEAK HEIGHT PERCENTAGE	4.84%	7.13%
CALCULATED STUTTER PEAK HEIGHT	72 RFUs	106 RFUs
REMAINDER ATTRIBUTABLE TO FOREIGN SOURCE	46 RFUs	12 RFUs
DEEMED ACCEPTABLE? (i.e., ≥100 RFUs)	No	No



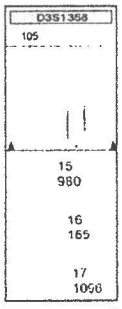
- Summary: Between the two samples, only Specimen #1-1 (SCF) would have been acceptable (and, at 100 RFU, barely so), and only under the assumption that the stutter from the 15 allele was no more than average. At a minimum, the two samples should not have been conflated together into a single conclusion, with a single statistic, to avoid misleading the reader.

D3S1358

#1-1 (SCF)	IF STUTTER IS AT AVERAGE PERCENTAGE	IF STUTTER IS AT MAXIMUM OBSERVED PERCENTAGE
PARENT PEAK HEIGHT (CALL)	1,011 RFUs (17)	1,011 RFUs (17)
QUESTIONED PEAK HEIGHT (CALL)	166 RFUs (16)	166 RFUs (16)
STUTTER PEAK HEIGHT PERCENTAGE	5.61%	9.4%
CALCULATED STUTTER PEAK HEIGHT	57 RFUs	95 RFUs
REMAINDER ATTRIBUTABLE TO FOREIGN SOURCE	109 RFUs	71 RFUs
DEEMED ACCEPTABLE? (i.e., ≥100 RFUs)	Yes	No



#1-2 (SCF)	IF STUTTER IS AT AVERAGE PERCENTAGE	IF STUTTER IS AT MAXIMUM OBSERVED PERCENTAGE
PARENT PEAK HEIGHT (CALL)	1,096 RFUs (17)	1,096 RFUs (17)
QUESTIONED PEAK HEIGHT (CALL)	165 RFUs (16)	165 RFUs (16)
STUTTER PEAK HEIGHT PERCENTAGE	5.61%	9.4%
CALCULATED STUTTER PEAK HEIGHT	61 RFUs	103 RFUs
REMAINDER ATTRIBUTABLE TO FOREIGN SOURCE	104 RFUs	62 RFUs
DEEMED ACCEPTABLE? (i.e., ≥100 RFUs)	Yes	No

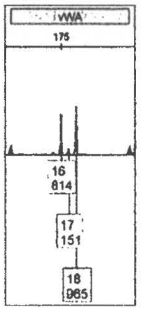


- Summary: Both Specimen #1-1 (SCF) and #1-2 (SCF) would have been acceptable, but only under the assumption that the stutter from the 15 allele was no more than average. If the stutter

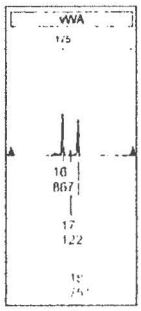
were just a little higher than average (6.63% for #1-1 and 6.02% for #1-2), then the neither would have been deemed acceptable. Extreme caution should have been employed here.

vWA

#1-1 (SCF)	IF STUTTER IS AT AVERAGE PERCENTAGE	IF STUTTER IS AT MAXIMUM OBSERVED PERCENTAGE
PARENT PEAK HEIGHT (CALL)	965 RFUs (18)	965 RFUs (18)
QUESTIONED PEAK HEIGHT (CALL)	151 RFUs (17)	151 RFUs (17)
STUTTER PEAK HEIGHT PERCENTAGE	5.58%	10.44%
CALCULATED STUTTER PEAK HEIGHT	54 RFUs	101 RFUs
REMAINDER ATTRIBUTABLE TO FOREIGN SOURCE	97 RFUs	50 RFUs
DEEMED ACCEPTABLE? (i.e., ≥100 RFUs)	No	No



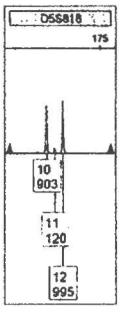
#1-2 (SCF)	IF STUTTER IS AT AVERAGE PERCENTAGE	IF STUTTER IS AT MAXIMUM OBSERVED PERCENTAGE
PARENT PEAK HEIGHT (CALL)	751 RFUs (18)	751 RFUs (18)
QUESTIONED PEAK HEIGHT (CALL)	122 RFUs (17)	122 RFUs (17)
STUTTER PEAK HEIGHT PERCENTAGE	5.58%	10.44%
CALCULATED STUTTER PEAK HEIGHT	42 RFUs	78 RFUs
REMAINDER ATTRIBUTABLE TO FOREIGN SOURCE	80 RFUs	44 RFUs
DEEMED ACCEPTABLE? (i.e., ≥100 RFUs)	No	No



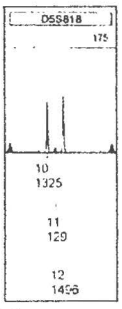
- Summary: The locus vWA should not have been reported for either of these samples, as the height of the 17 allele was due, in part, to stutter from the 18 allele.

D5S818

#1-1 (SCF)	IF STUTTER IS AT AVERAGE PERCENTAGE	IF STUTTER IS AT MAXIMUM OBSERVED PERCENTAGE
PARENT PEAK HEIGHT (CALL)	995 RFUs (12)	995 RFUs (12)
QUESTIONED PEAK HEIGHT (CALL)	120 RFUs (11)	120 RFUs (11)
STUTTER PEAK HEIGHT PERCENTAGE	4.29%	7.57%
CALCULATED STUTTER PEAK HEIGHT	43 RFUs	75 RFUs
REMAINDER ATTRIBUTABLE TO FOREIGN SOURCE	77 RFUs	45 RFUs
DEEMED ACCEPTABLE? (i.e., ≥100 RFUs)	No	No



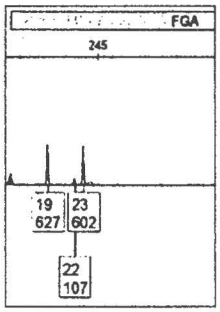
#1-2 (SCF)	IF STUTTER IS AT AVERAGE PERCENTAGE	IF STUTTER IS AT MAXIMUM OBSERVED PERCENTAGE
PARENT PEAK HEIGHT (CALL)	1,496 RFUs (12)	1,496 RFUs (12)
QUESTIONED PEAK HEIGHT (CALL)	129 RFUs (11)	129 RFUs (11)
STUTTER PEAK HEIGHT PERCENTAGE	4.29%	7.57%
CALCULATED STUTTER PEAK HEIGHT	64 RFUs	113 RFUs
REMAINDER ATTRIBUTABLE TO FOREIGN SOURCE	65 RFUs	16 RFUs
DEEMED ACCEPTABLE? (i.e., ≥100 RFUs)	No	No



- Summary: The locus D5S818 should not have been reported for either of these samples, as the height of the 17 allele was due, in part, to stutter from the 18 allele.

FGA

#1-1 (SCF)	IF STUTTER IS AT AVERAGE PERCENTAGE	IF STUTTER IS AT MAXIMUM OBSERVED PERCENTAGE
PARENT PEAK HEIGHT (CALL)	602 RFUs (23)	602 RFUs (23)
QUESTIONED PEAK HEIGHT (CALL)	107 RFUs (22)	107 RFUs (22)
STUTTER PEAK HEIGHT PERCENTAGE	6.37%	11.2%
CALCULATED STUTTER PEAK HEIGHT	38 RFUs	67 RFUs
REMAINDER ATTRIBUTABLE TO FOREIGN SOURCE	69 RFUs	40 RFUs
DEEMED ACCEPTABLE? (i.e., ≥100 RFUs)	No	No



- Summary: The locus D5S818 should not have been reported for either of these samples, as the height of the 17 allele was due, in part, to stutter from the 18 allele.

In summary, of these five loci:

- Three loci should not have been accepted as a matter of course (vWA, D5S818, and FGA), as their legitimacy, under the lab's own protocols, was artificially elevated by stutter, and using only the average stutter value. Therefore, they should not have been reported and replaced with an asterisk, as they did not meet the laboratory's reporting threshold, as was done with other loci.
- The remaining two loci (D8S1179 and D3S1358), while acceptable with consideration to the average stutter value, were not beyond the maximum stutter percentages, and could not be reliably deemed as being acceptable or not.

Consequently, the sixth allele (TH01:8) is the only locus that remains viable for consideration.

24. Manipulation of the Statistical Frequencies – As stated in my letter dated 05/07/14 (see Exhibit B), *"Six loci were used in the statistical calculation that was reported by the New Jersey State Police's Office of Forensic Sciences on 11/01/11 (D8S1179, D3S1358, TH01, D13S317, vWA, and D5S818)."* A simple observation would have noted that, of these six loci, only five are the same as the loci that bore foreign alleles, that FGA was removed, and that D13S317 was added. This simple swap had a significant impact on the statistical calculations.

25. The removal of FGA – FGA was not used in the statistical calculations, but there is no explanation as to why. One possible reason is that the inclusion of this locus would have resulted in the defendant being excluded. To wit, the three alleles detected at FGA for Specimen #1-1 (SCF) were 19, 23, and (22); the 19 and 23 could have come from the complainant herself, thus leaving the 22 as foreign. If those three alleles were used in the calculations, then the computed number would have reflected the portion of the population that could have been contributors to this sample, which are the heterozygous pairs [19, 22], [22, 23], and [19, 23], as well as the homozygous pairs of [19, 19], [22, 22], and [23, 23]; any individual who had one of those pairs of alleles could not be excluded as a

possible contributor. The defendant, however, being [22, 24], is not one of those pairs, and would therefore have been excluded. By omitting the inconvenient locus, the statistical calculation was tailored to that of the defendant. Dr. Peter Gill, *et al.*, said it best in a 2006 article entitled "DNA commission of the International Society of Forensic Genetics: Recommendations on the interpretation of mixtures:: *"We have seen many instances in which laboratories do just this, usually by omitting from the RMNE calculation the inconvenient loci. Such a calculation implies, certainly incorrectly, that among the "random men" considered for comparison by the calculation only the same loci would be used for inculpation/exculpation as those being considered for the present suspect. It fails to acknowledge that choosing the omitted loci is suspect-centric and therefore prejudicial against the suspect."* (P. Gill, *et al.*, Forensic Science International 160 (2006) 90–101; see Exhibit F). The following is an excerpt from page 5 of the analyst's case notes, which shows the six loci that were used in the statistical calculation of the combination of Specimens #1-1 (SCF) and #1-2 (SCF), showing that, in the table marked "Mixture," the six loci and their alleles are:

- D8S1179: 10, 14, and 15
- D3S1358: 15, 16, and 17
- TH01: 6 and 8
- D13S317: 9 and 12
- vWA: 16, 17, and 18
- D5S818: 10, 11, and 12

NJSP DNA LABORATORY
Two Person Mixture - Likelihood Ratio
Allele frequencies obtained from:
(JFS Vol 46, No. 3 May 2001)
(JFS Vol 48, No. 4 July 2003) for D2 & D19

Hypotheses:
LR = The mixture is Spec.# 1-5 and Spec.# 2 / The mixture is Spec.#1-5 and some unknown contributor

Lab No. C11-00029 Supplemental
Specimens # 1-5 (V), 2 (S) and 1-1 (SCF)(V), 1-2 (SCF) (V)

Analyst: TJN
Date: November 1, 2011

	Mixture				Reference		Unknown					
	Spec.# 1-1 (SCF), 1-2 (SCF)				Spec.# 1-5		Combination 1		Combination 2		Combination 3	
Locus	Allele 1	Allele 2	Allele 3	Allele 4	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2
D8S1179	10	14	15		10	15	10	14	14	14	14	15
D21S11					28	33.2						
D7S820					9	9						
CSF1PO					12	12						
D3S1358	15	16	17		15	17	15	16	16	16	16	17
TH01	6	8			6	6	6	8	8	8		
D13S317	9	12			9	12	9	9	9	12	12	12
D16S539					9	11						
D2S1338					18	20						
D19S433					14	14						
vWA	16	17	18		16	18	16	17	17	17	17	18
TPOX					8	11						
D18S51					15	17						
D5S818	10	11	12		10	12	10	11	11	11	11	12
FGA					19	23						

	African-American	Caucasian	Hispanic
Total Likelihood Ratio	9.099E+03	1.906E+04	1.411E+04
	9.09 thousand	19 thousand	14.1 thousand

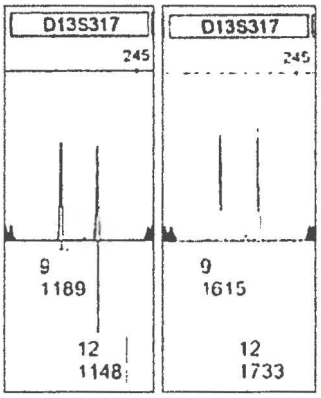
Thus, FGA was clearly omitted from the calculation. However, in her report dated 11/01/11, there is no conditional language to reflect this omission:

> **CONCLUSIONS & INTERPRETATIONS**
>
> A mixture of DNA profiles was identified in Specimens No. 1-1 (SCF) and 1-2 (SCF). Emily Strife and Shawn D. Shaw cannot be excluded as partial contributors to the mixed DNA profile obtained. Assuming two contributors, one of whom is Emily Strife, it is approximately:
>
> 9.09 thousand times more likely in the African-American population
> 19.0 thousand times more likely in the Caucasian population
> 14.1 thousand times more likely in the Hispanic population
>
> that the source of the mixed DNA profile is Emily Strife and Shawn D. Shaw rather than Emily Strife and a randomly selected individual.

26. The inclusion of D13S317 – There were only two alleles that were detected at D13S317, a 9 and a 12, which are the same two that the complainant has; there were no foreign alleles detected that indicated the presence of another individual. Meanwhile, the defendant has two 12 alleles at this locus:

Specimen No.	Specimen Description	Human DNA Probe	D8S1179	D21S11	D7S820	CSF1PO	D3S1358	TH01	D13S317	D16S539	D2S1338	D19S433	vWA	TPOX	D18S51	Amelogenin	D5S818	FGA
2	Buccal Swab Reference (S)	+	14,15	30,32	10,11	10,13	16,17	8,8	12,12	11,12	21,23	12,14	17,18	7,8	15,19	X,Y	11,12	22,24
1-5	Buccal Swab Reference (V) (Previously reported 5/2/11)		10,15	28,33.2	9,9	12,12	15,17	6,6	9,12	9,11	18,20	14,14	16,18	8,11	15,17	X,X	10,12	19,23
1-1 (SCF)	Vaginal Swabs (V) (Previously reported 5/2/11)		10,15 (14)	28,33.2*	9,9	12,12	15,17 (16)	6.6 (8)	9,12	9,11	18,20	14,14*	16,18 (17)	8,11	15,17	X,X*	10,12 (11)	19,23 (22)
1-1	Vaginal Swabs (V) (Previously																	

The following are excerpts from pages 29 (Specimen #1-1 (SCF), left; see Exhibit G) and 32 (Specimen #1-2 (SCF), right; see Exhibit H) of the analyst's notes, which shows the electropheragrammic data for the locus in question:



The height of an allele's peak is a relative indication of its quantity. At D13S317, the heights of the 9 and 12 alleles are almost equal and do not indicate that a homozygous 12 contributor is clearly present. This situation, where one person's alleles are identical to, or inclusive of, another person's, is known as "masking."

The inclusion of D13S317 into the statistical calculations is profound. It is the only locus where the complainant's alleles masked the defendant. By including this locus into the statistical calculations, the statistical frequencies were artificially elevated against the defendant. Without it, the statistical frequencies dropped to 1,860 (see Paragraph 19 for more details), according Ms. Nezezon.

The following is an excerpt from page 5 of the analyst's case notes, which shows the six loci that were used in the statistical calculation of the combination of Specimens #1-1 (SCF) and #1-2 (SCF), showing that, in the table marked "Mixture," that the six loci and their alleles are:

- D8S1179: 10, 14, and 15
- D3S1358: 15, 16, and 17
- TH01: 6 and 8
- D13S317: 9 and 12
- vWA: 16, 17, and 18
- D5S818: 10, 11, and 12

NJSP DNA LABORATORY
Two Person Mixture - Likelihood Ratio
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Hypotheses:
LR = The mixture is Spec.# 1-5 and Spec.# 2 / The mixture is Spec.#1-5 and some unknown contributor

Lab No. C11-00029 Supplemental
Specimens # 1-5 (V), 2 (S) and 1-1 (SCF)(V), 1-2 (SCF) (V)

Analyst: TJN
Date: November 1, 2011

	Mixture				Reference		Unknown					
	Spec.# 1-1 (SCF), 1-2 (SCF)				Spec.# 1-5		Combination 1		Combination 2		Combination 3	
Locus	Allele 1	Allele 2	Allele 3	Allele 4	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2
D8S1179	10	14	15		10	15	10	14	14	14	14	15
D21S11					28	33.2						
D7S820					9	9						
CSF1PO					12	12						
D3S1358	15	16	17		15	17	15	16	16	16	16	17
TH01	6	8			6	6	6	8	8	8		
D13S317	9	12			9	12	9	9	9	12	12	12
D16S539					9	11						
D2S1338					18	20						
D19S433					14	14						
vWA	16	17	18		16	18	16	17	17	17	17	18
TPOX					8	11						
D18S51					15	17						
D5S818	10	11	12		10	12	10	11	11	11	11	12
FGA					19	23						

	African-American	Caucasian	Hispanic
Total Likelihood Ratio	9.099E+03	1.906E+04	1.411E+04
	9.09 thousand	19 thousand	14.1 thousand

The inclusion of D13S317 means that the software considered individuals who were either the heterozygous [9,12] or the homozygous [9,9] – neither of which is consistent the defendant. The homozygous [12,12] is, however – but there is no indication in the electropheragram to indicate that there is anything but the complainant's alleles, which is the heterozygous [9,12]. Thus, by

consciously including this locus into the calculation, the program generated a number that was artificially elevated against the defendant.

27. Forensic DNA Y-STR Analysis – I have not been provided a copy of the testimonies of any scientific experts in the instant case, nor was I present at trial to hear the testimonies of any experts. Hence, I do not know if the advantages and disadvantages of forensic Y-STR analysis was ever explained. For the purposes of this affidavit, I must assume that they did not.

28. Y-STRs are short tandem repeat (STR) sequences that are only known to occur on the Y chromosome, which is the male chromosome. In fact, these sequences are so unique, that it is believed that they do not occur anywhere else on Earth, in any other form of life, save that of the males of the upper primates. Because the Y chromosome is inherited directly from the father without any interference by the mother, the son inherits an exact copy of his father's Y chromosome. Consequently, the Y-STR DNA profiles of the father and the son are identical because the Y chromosome is identical. By extension of that logic, two sons of the same father will also have identical Y-STR profiles, as will the sons of the son (*i.e.*, grandsons), as will the sons of the sons (*i.e.*, male cousins). This is the reason why the DNA Laboratory Report #C11-00029 Supplemental (dated 06/08/15) and Amended Supplemental (dated 06/15/15) specify that *"due to the paternal inheritance of YSTR DNA, it is expected that all his paternal male relatives cannot be excluded as possible contributors to the Y-STR DNA profile obtained"* in the conclusion for Specimens No. 1-4 (SCF) and 1-2 (SCF). Consequently, it is entirely possible for two male strangers to share the same Y-STR DNA profile, because they are direct male descendants of a common male ancestor.

29. A 2014 article entitled "A substantially lower frequency of uninformative matches between 23 versus 17 Y-STR haplotypes in north Western Europe" (M.H.D. Larmuseau, *et al.*, Forensic Science International: Genetics 11 (2014) 214–219; see Exhibit I) summarizes the situation by saying, *"Based on this data and the results of this study, it is clear that familial DNA searching based on 23 Y-STR haplotypes is much more promising than before when based on the 17 Y-STR as the number of false positive (near) matches decreases substantially."* Consequently, companies released enhanced kits, like Applied Biosystems' Yfiler Plus kit, which analyzed 23 genetic markers and was commercially available at the time of trial.

30. A 2017 article entitled "Case report: Coincidental inclusion in a 17-locus Y-STR mixture, wrongful conviction and exoneration" (G. Hampikian, *et al.*, Forensic Science International: Genetics 31 (2017) 1–4; see Exhibit J), states the issue very simply, in a real-world post-conviction example: *"This case demonstrates how a coincidental Y-STR DNA mixture inclusion, with match statistics favoring a prosecution hypothesis, can lead to an erroneous conviction. The report shows the*

importance of considering all relevant hypotheses to explain DNA mixtures, and the importance of communicating these possible interpretations to interested parties including the triers-of-fact. It also demonstrates the power of using more Y- STR markers to discriminate between alternative mixture hypotheses. To our knowledge, this is the first published report of an overturned wrongful conviction based on coincidental Y-STR mixture. It is beyond the scope of this paper to estimate the frequency of such coincidental matches that have resulted in wrongful convictions."

31. Verbal Scale – I have not been provided a copy of Ms. Nezezon's declaration, so I do not know what *"seminal DNA textbook"* the State's Brief is referring to. The verbal scale equivalent is a qualitative assessment of a quantitative measure, *i.e.*, the likelihood ratio. The following is an excerpt from "The impact of the principles of evidence interpretation on the structure and content of statements" (Science & Justice 2000; 40(4):233-239; see Exhibit K), where Dr. Ian Evett shares the scale used by the Forensic Science Service, London, UK:

Verbal scale

In the FSS, weight of evidence is communicated by the use of the word *supports* together with an appropriate qualifier, chosen from the list: *limited, moderate, moderately strong, strong, very strong*. The equivalence between numbers and words is a matter to be settled by consensus among scientists from all disciplines. At the present time the verbal convention followed by the FSS is as follows

LR	
>1 to 10	Limited evidence to support
10 to 100	Moderate evidence to support
100 to 1000	Moderately strong evidence to support
1000 to 10000	Strong evidence to support
> 10000	Very strong evidence to support

This reference, however, would have ranked a likelihood ratio of 1,860 as *"strong"* support, not *"very strong support,"* as per the Brief. It should be noted that Dr. Evett follows with this warning: *"Of course, the divisions in the table cannot be seen as arbitrary discontinuous steps. It would be ludicrous to claim that a likelihood ratio of 999 is materially different in its impact from one of 1001: but that kind of precision is rarely realistic in forensic science and the scale is no more than a guide to the judgement [sic] of the scientist."* He then concludes by saying, *"It is understandable that our customers may ask to have a brief conclusion containing a simply stated "bottom line". But we can easily see that this is a simplistic view. For example, our "bottom line" might be strong support for a level I proposition. A hurried prosecutor may not sense the issues that need to be addressed in considering the level 3 propositions that will be before the court."*

Verbal scale equivalents are not uniform. The following is an excerpt from page 64 of the "European Network of Forensic Science Institutes Guideline for Evaluative Reporting in Forensic

Science: Strengthening the Evaluation of Forensic Results Across Europe" (2015, see Exhibit L), which a likelihood ratio of 1,860 would also have garnered a *"strong support"* statement:

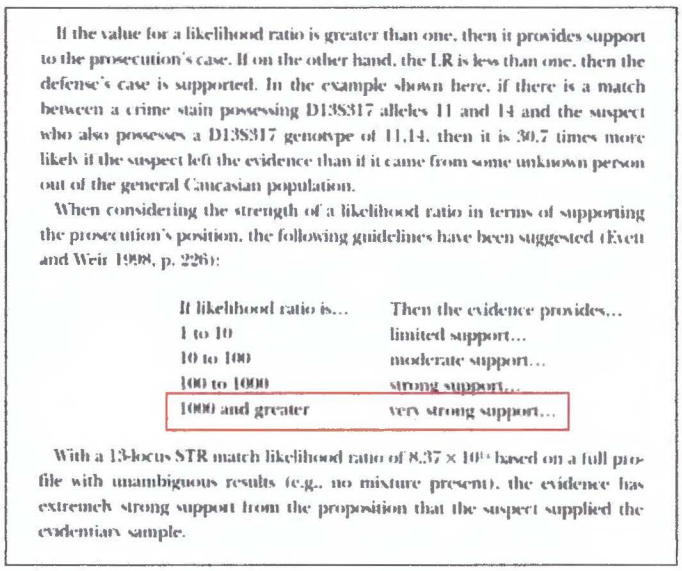
Supported proposition	Verbal scale	LR
First proposition is supported against the alternative proposition	Slight support /Limited support	1 < LR ≤ 10
	Moderate support	10 < LR ≤ 100
	Moderately strong support	100 < LR ≤ 1000
	Strong support	1000 < LR ≤ 10000
	Very strong support	LR > 10000
The alternative proposition is supported against the first proposition	Slight support /Limited support	0.1 ≤ LR < 1
	Moderate support	0.01 ≤ LR < 0.1
	Moderately strong support	0.001 ≤ LR < 0.01
	Strong support	0.0001 ≤ LR < 0.001
	Very strong support	LR < 0.0001

It may be tempting to dismiss the ENFSI guidelines as inapplicable to the United States. The Scientific Working Group on DNA Analysis Methods (SWGDAM) is an independent group that issues guidelines and standards for best practices in forensic DNA analysis in the United States. The following is an excerpt from page 3 of the "Recommendations of the SWGDAM Ad Hoc Working Group on Genotyping Results Reported as Likelihood Ratios" (2018; see Exhibit M), which would have ranked a likelihood ratio of 1,860 as merely *"moderate support"*:

Table 1. **Scale of verbal qualifiers for reporting likelihood ratios**

***LR* for H_p Support and 1/*LR* for H_d Support**	**Verbal Qualifier**
1	Uninformative
2 – 99	Limited Support
100 – 9,999	Moderate Support
10,000 – 999,999	Strong Support
≥1,000,000	Very Strong Support

32. In his book, Forensic DNA Typing (second edition, Elsevier Academic Press, 2005; see Exhibit N), Dr. John Butler offers that a likelihood ratio of 1,000 and greater to be *"very strong support"*:



If the value for a likelihood ratio is greater than one, then it provides support to the prosecution's case. If on the other hand, the LR is less than one, then the defense's case is supported. In the example shown here, if there is a match between a crime stain possessing D13S317 alleles 11 and 14 and the suspect who also possesses a D13S317 genotype of 11,14, then it is 30.7 times more likely if the suspect left the evidence than if it came from some unknown person out of the general Caucasian population.

When considering the strength of a likelihood ratio in terms of supporting the prosecution's position, the following guidelines have been suggested (Evett and Weir 1998, p. 226):

If likelihood ratio is...	Then the evidence provides...
1 to 10	limited support...
10 to 100	moderate support...
100 to 1000	strong support...
1000 and greater	very strong support...

With a 13-locus STR match likelihood ratio of 8.37×10^{11} based on a full profile with unambiguous results (e.g., no mixture present), the evidence has extremely strong support from the proposition that the suspect supplied the evidentiary sample.

It should be noted, however, that he adds that this is based on *"a full profile with unambiguous results (e.g., no mixture present)..."*. This will be a relevant and significant distinction in Paragraph 35.

33. In his book, Forensic DNA Evidence Interpretation (CRC Press, 2005; see Exhibit O), Dr. John Buckleton, *et al.*, offer that a likelihood ratio of 1,000 and greater to be *"moderately strong support"*:

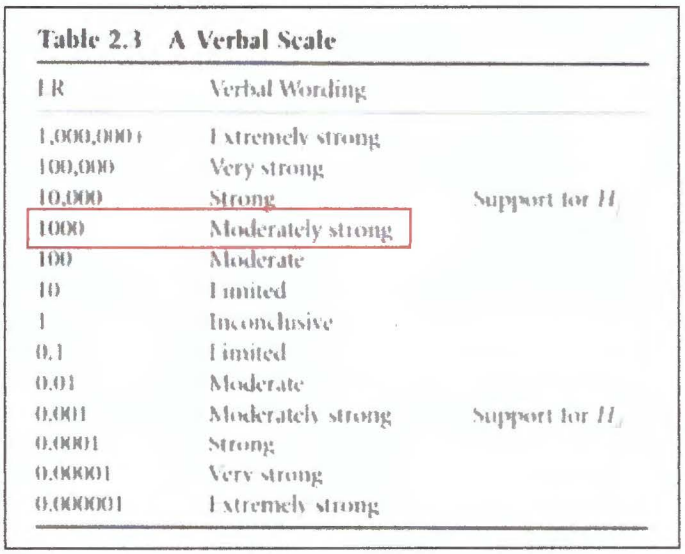


Table 2.3 A Verbal Scale

LR	Verbal Wording	
1,000,000+	Extremely strong	
100,000	Very strong	
10,000	Strong	Support for H_1
1000	Moderately strong	
100	Moderate	
10	Limited	
1	Inconclusive	
0.1	Limited	
0.01	Moderate	
0.001	Moderately strong	Support for H_2
0.0001	Strong	
0.00001	Very strong	
0.000001	Extremely strong	

It should be very clear by now that there is no universally accepted scale of statements in the forensic science industry, much less in forensic DNA analysis.

34. **In fact, the use of verbal scale equivalents are not even a universally accepted practice in the forensic sciences, due to their persuasive effect on the lay person, combined with their illusion of precision.** In "What should a forensic practitioner's likelihood ratio be?" (Science and Justice 56 (2016) 374–379; see Exhibit P), authors Morrison and Enziger write, *"More substantially, expressions such as*

"slightly more probable", "more probable", "appreciably more probable", "much more probable", "far more probable" and "exceedingly more probable" (Willis et al. [36]) are vague and will be interpreted differently by different individuals. Their meaning can only be made explicit via reference to their associated ranges of likelihood ratio values, e.g., 2–10, 10–100, 100–1000, 1000–10,000, 10,000–1,000,000, 1,000,000+, and an explanation of what a likelihood ratio is, what it means, and how it normatively should be used. Transparency is essential and an explanation has to be given, the use of a verbal expression instead of a numeric value obfuscates rather than clarifies." They conclude by saying, *"Forensic scientists should evaluate and quantify strength of evidence in a manner which they believe to be logically correct and for which they can provide suitable warrant. Without compromising the latter, we also need to be concerned about transparency and how best to communicate our strength of evidence conclusions to the court."*

To conclude, it should be quite evident that calling the modified statistical frequency *"very strong support"* is weak, and that is without even considering the legitimacy of the loci that were used in the calculation (see Paragraphs 21 and 23).

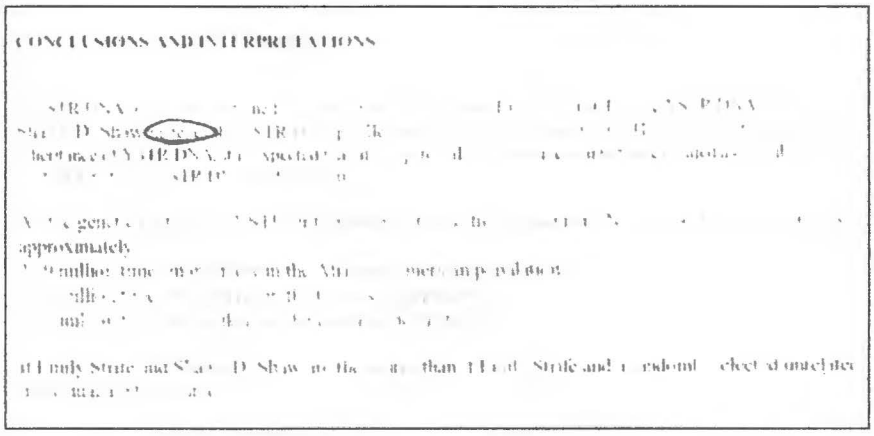
35. Combining STR and Y-STR frequencies – The State's Brief goes on to say, *"Furthermore, when multiplied by the likelihood ratio from the YSTR analysis, the combined likelihood ratio is 5.94 million, as compared to the 28.9 million likelihood ratio calculated with the D13S17 [sic] locus. Id. ¶ 6. Accordingly, even if defense counsel had cross-examined Nezezon regarding the inclusion of D13S17 [sic] or Young had testified about this possibly erroneous inclusion, Shaw was not prejudiced because the DNA evidence against him alone would still be overwhelming."* In my email (see Exhibit C), I had said, *"If the NJSP lab wants to use this method, they have some support in this field."* I was referring to Section 10.5.1 of the SWGDAM Interpretation Guidelines for Y-Chromosome STR Typing by Forensic DNA Laboratories (see Exhibit Q), which was approved by the Scientific Working Group on DNA Analysis Methods on 01/09/14, and states:

> **10.5.1 Combining autosomal and Y-STR results requires a consistent approach to the statistical question being addressed. Under the assumption of negligible dependencies, the match probability formula (Eq. 3) is to be multiplied by the autosomal match probability as defined by National Research Council (1996) Recommendation 4.2.**

However, it specifically states that *"the match probability formula (Eq. 3) is to be multiplied by the autosomal match probability"*. In a single and simple sentence, the match probability is the odds of randomly selecting someone from a given population with a particular DNA profile. For STRs, the

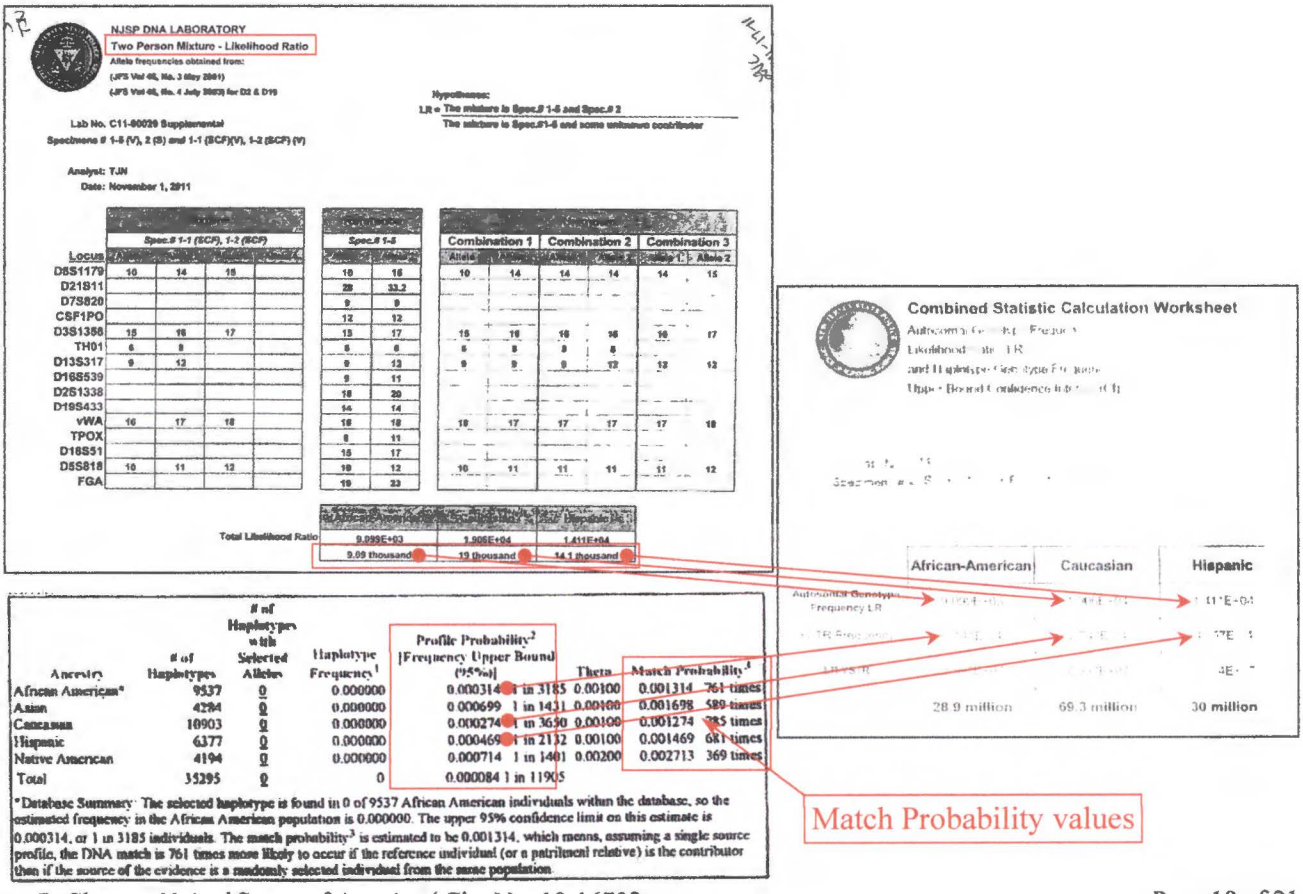
issue is fairly straightforward. For Y-STRs, however, the frequency of a particular profile is dependent on how many sons a man has, and how quickly his progeny reproduce.

The following is an excerpt from page 1 of the DNA Laboratory Report #C11-00029 Supplemental (dated 06/08/15), which combined the STR (*i.e.*, autosomal) and Y-STR data into a single statistical frequency:



CONCLUSIONS AND INTERPRETATIONS

The reported statistical frequencies were generated on page 9 of the analyst's notes dated 06/08/15 (right), which combined the STR (*i.e.*, autosomal; top left; page 5) and Y-STR (bottom left; page 6) into a single statistical frequency (see Exhibit R):



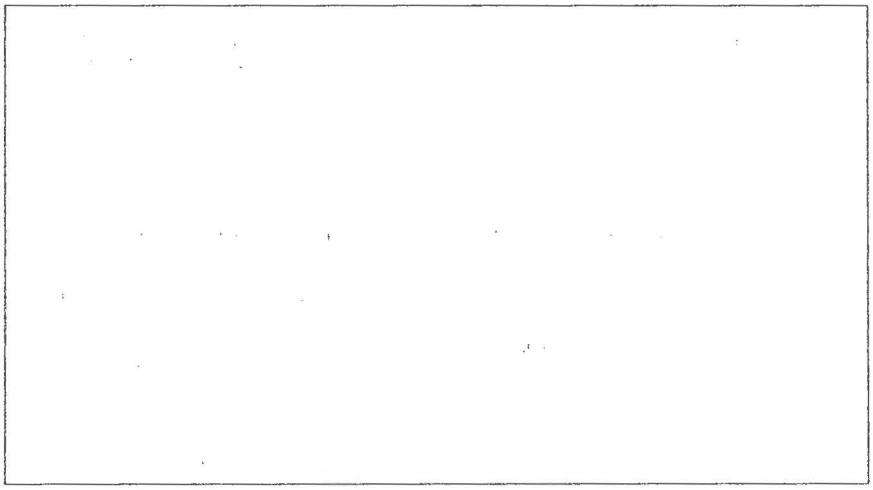
It should be noted that the above Y-STR frequencies are for Specimen #1-1 (SCF), whereas a separate frequency was generated for Specimen #1-2 (SCF), which had a different match probability and would, therefore, generate a different statistical frequency (see Exhibit R):

Ancestry	# of Haplotypes	# of Haplotypes with Selected Alleles	Haplotype Frequency[1]	Profile Probability[2] [Frequency Upper Bound (95%)]		Theta	Match Probability[3]	
African American*	9537	0	0.000000	0.000314	1 in 3185	0.00060	0.000914	1094 times
Asian	4284	0	0.000000	0.000699	1 in 1431	0.00060	0.001299	770 times
Caucasian	10903	0	0.000000	0.000274	1 in 3650	0.00060	0.000874	1144 times
Hispanic	6377	0	0.000000	0.000469	1 in 2132	0.00060	0.001069	936 times
Native American	4194	0	0.000000	0.000714	1 in 1401	0.00200	0.002713	369 times
Total	35295	0	0	0.000084	1 in 11905			

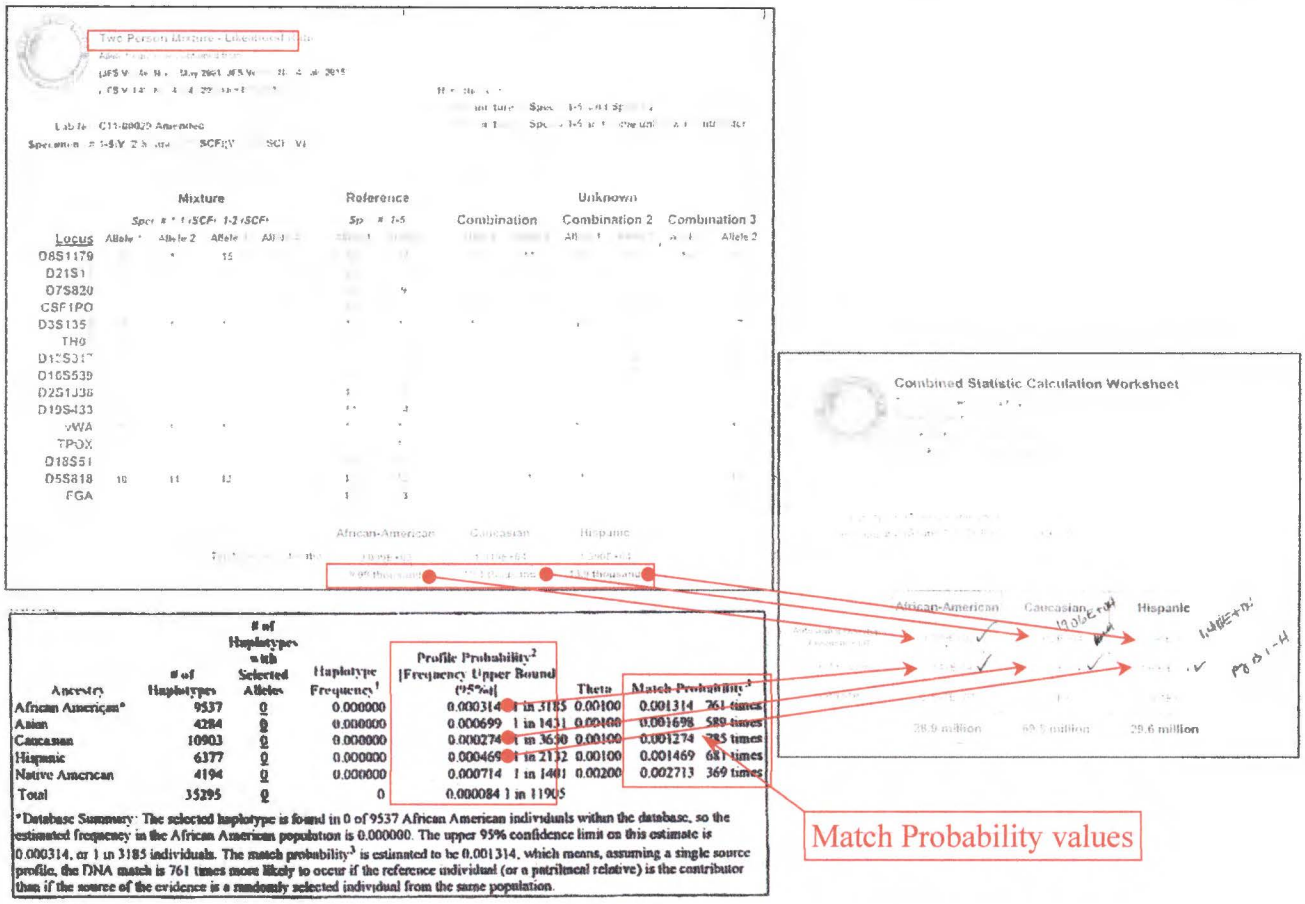
*Database Summary: The selected haplotype is found in 0 of 9537 African American individuals within the database, so the estimated frequency in the African American population is 0.000000. The upper 95% confidence limit on this estimate is 0.000314, or 1 in 3185 individuals. The match probability[3] is estimated to be 0.000914, which means, assuming a single source profile, the DNA match is 1094 times more likely to occur if the reference individual (or a patrilineal relative) is the contributor than if the source of the evidence is a randomly selected individual from the same population.

The statistical frequency that was issued with the STRs, however, was not a match probability for a single contributor, but a likelihood ratio for a mixture of at least two contributors; therefore, the method employed is not prescribed by SWGDAM (see Exhibit Q) nor Dr. Butler (see Paragraph 32). Furthermore, the Y-STR values that were entered were that of the profile probability, not the match probability, as prescribed by the SWGDAM guidelines. The reported values are, therefore, both (a) incorrectly calculated and (b) not what was proffered in the report.

36. The above report was superseded by an Amended Supplemental report, dated 06/15/15:



The reported statistical frequencies were generated on page 4 of the analyst's notes dated 06/15/15 (right), which combined the STR (*i.e.*, autosomal; top left; page 5) and Y-STR (bottom left; page 6) into a single statistical frequency (see Exhibit S):



Consequently, the *"corrected statistics"* refer to the *erratum* that was published by the FBI in 2001, which corrected the allelic frequencies that were reported in 1999 – they do not refer to the incorrect use of the profile probability instead of match probability, nor the incorporation of a likelihood ratio instead of a match probability, nor any of the other issues addressed in this affidavit.

The above statement and the information contained in the attached curriculum vitae are accurate to the best of my knowledge and belief.

Further, the affiant saith not.

Mr. Arthur W. Young, B.S., F-ABC
Guardian Forensic Sciences
Abington, PA

Sworn to and subscribed before me
this 10 day of December, 2020.

Notary Public
My Commission Expires: June 30, 2022

Commonwealth of Pennsylvania - Notary Seal
LILIAN M SHAPIRO - Notary Public
Montgomery County
My Commission Expires Jun 30, 2022
Commission Number 1284482